

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/029,016DATE: 01/25/2002
TIME: 05:50:37

INPUT SET: S36729.raw

#2

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: WOZNEY, John
CELESTE, Anthony J.
THIES, R. Scott

(ii) TITLE OF INVENTION: BMP-11 COMPOSITIONS

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: GENETICS INSTITUTE, INC.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10/029,016
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/414,234
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MEINERT, M.C.
(B) REGISTRATION NUMBER: 31,544
(C) REFERENCE/DOCKET NUMBER: GI5205-B

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617 876-1170
(B) TELEFAX: 617 876-5851

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 789 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: double
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: DNA (genomic)
57
58 (vi) ORIGINAL SOURCE:
59 (A) ORGANISM: Bos Taurus
60 (B) STRAIN: Bovine Activin WC
61
62 (ix) FEATURE:
63 (A) NAME/KEY: CDS
64 (B) LOCATION: 324..704
65
66 (ix) FEATURE:
67 (A) NAME/KEY: misc_feature
68 (B) LOCATION: 322..323
69 (D) OTHER INFORMATION: /note= "putative 3' end of intron"
70
71 (ix) FEATURE:
72 (A) NAME/KEY: mat_peptide
73 (B) LOCATION: 375..701
74
75
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
77
78 A A A C T G T A T T T T G G G G T G A A G G T G T G A G T T A A T A G A T T C A C G G G A C A A C A A A G A T G G G C T 60
79
80 G T T G T T G A G A C C T T G G G C C A A G G G G C T G A T G A G G G T C A G G T T G C C A A G A G A G A G A G A A T T 120
81
82 A G G G A A G G T G A G T T A G G G A G A C A T G G C T A G C T G G C A A G A A A G T G G G T A G A A A C A G G G 180
83
84 G T T G G G G A G G G G A G C A C T G G A G A A G C T C A G A A A T C A C T T G G T C T C T G T T C T C C T G C C C C T 240
85
86 A C T G A G G G G C A G G T G A G A A G A A C A G G G A G T A G G A G C T C C T C G A G G C T C T A T T A C A T C T C 300
87
88 T T T C T C C T C T C C C T C A C C C C C A G C A T C C T T T A T G G A G C T T C G A G T C C T A 350
89 His Pro Phe Met Glu Leu Arg Val Leu
90 -17 -15 -10
91
92 G A G A A C A C A A A C G G T C C C G G C G G A A C C T G G G C C T G A C T G C G A T G A A 398
93 Glu Asn Thr Lys Arg Ser Arg Arg Asn Leu Gly Leu Asp Cys Asp Glu
94 -5 1 5
95
96 C A T T C A A G T G A G T C C C G C T G T T G C C G C T A C C C C T C A C T G T G A C T T T 446
97 His Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe
98 10 15 20
99

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100 GAG GCT TTT GGC TGG GAC TGG ATC ATC GCT CCT AAA CGC TAC AAG GCC 494
101 Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala
102 25 30 35 40
103
104 AAC TAC TGC TCC GGC CAG TGC GAG TAC ATG TTT ATG CAA AAG TAT CCG 542
105 Asn Tyr Cys Ser Gly Gln Cys Glu Tyr Met Phe Met Gln Lys Tyr Pro
106 45 50 55
107
108 CAC ACC CAC TTG GTG CAA CAG GCT AAC CCA AGA GGC TCT GCG GGG CCC 590
109 His Thr His Leu Val Gln Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro
110 60 65 70
111
112 TGC TGC ACA CCC ACC AAG ATG TCC CCA ATC AAC ATG CTC TAC TTC AAT 638
113 Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn
114 75 80 85
115
116 GAC AAG CAG CAG ATT ATC TAC GGC AAG ATC CCT GGC ATG GTG GTG GAT 686
117 Asp Lys Gln Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val Val Asp
118 90 95 100
119
120 CGC TGT GGC TGC TCC TAAGGTGGGG GACAGCGGAT GCCTCCCCAA CAGACCCTGC 741
121 Arg Cys Gly Cys Ser
122 105
123
124 CCCTAGACTC CCCCAGCCCT GACCCCTGC TCCCCGGCCC TAGAGCTC 789
125
126
127 (2) INFORMATION FOR SEQ ID NO:2:
128
129 (i) SEQUENCE CHARACTERISTICS:
130 (A) LENGTH: 126 amino acids
131 (B) TYPE: amino acid
132 (D) TOPOLOGY: linear
133
134 (ii) MOLECULE TYPE: protein
135
136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
137
138 His Pro Phe Met Glu Leu Arg Val Leu Glu Asn Thr Lys Arg Ser Arg
139 -17 -15 -10 -5
140
141 Arg Asn Leu Gly Leu Asp Cys Asp Glu His Ser Ser Glu Ser Arg Cys
142 1 5 10 15
143
144 Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp
145 20 25 30
146
147 Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Gln Cys
148 35 40 45
149
150 Glu Tyr Met Phe Met Gln Lys Tyr Pro His Thr His Leu Val Gln Gln
151 50 55 60
152

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153 Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met
154      65                      70                      75
155
156 Ser Pro Ile Asn Met Leu Tyr Phe Asn Asp Lys Gln Gln Ile Ile Tyr
157      80                      85                      90                      95
158
159 Gly Lys Ile Pro Gly Met Val Val Asp Arg Cys Gly Cys Ser
160      100                      105
161
162

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (B) STRAIN: Human Activin WC

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..183

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 184..185
- (D) OTHER INFORMATION: /note= "two-thirds of codon at end of partial clone"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

190 TCTAGATGCT CCGGCCAGTG CGAGTAC ATG TTC ATG CAA AAA TAT CCG CAT      51
191      Met Phe Met Gln Lys Tyr Pro His
192      1                      5
193
194 ACC CAT TTG GTG CAG CAG GCC AAT CCA AGA GGC TCT GCT GGG CCC TGT      99
195 Thr His Leu Val Gln Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys
196      10                      15                      20
197
198 TGT ACC CCC ACC AAG ATG TCC CCA ATC AAC ATG CTC TAC TTC AAT GAC      147
199 Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Asp
200      25                      30                      35                      40
201
202 AAG CAG CAG ATT ATC TAC GGC AAG ATC CCT GGC ATG GTGGTGGATC      193
203 Lys Gln Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met
204      45                      50
205

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PATENT APPLICATION US/10/029,016DATE: 01/25/2002
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213

206 GCTGTGGCTG CTCCGGATCC

207

208

209 (2) INFORMATION FOR SEQ ID NO:4:

210

211 (i) SEQUENCE CHARACTERISTICS:

212 (A) LENGTH: 52 amino acids

213 (B) TYPE: amino acid

214 (D) TOPOLOGY: linear

215

216 (ii) MOLECULE TYPE: protein

217

218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

219 Met Phe Met Gln Lys Tyr Pro His Thr His Leu Val Gln Gln Ala Asn
220 1 5 10 15

221

222 Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro
223 20 25 30

224

225 Ile Asn Met Leu Tyr Phe Asn Asp Lys Gln Gln Ile Ile Tyr Gly Lys
226 35 40 45

227

228 Ile Pro Gly Met
229 50

230

231

232 (2) INFORMATION FOR SEQ ID NO:5:

233

234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 30 base pairs

236 (B) TYPE: nucleic acid

237 (C) STRANDEDNESS: single

238 (D) TOPOLOGY: linear

239

240 (ii) MOLECULE TYPE: DNA (genomic)

241

242 (vi) ORIGINAL SOURCE:

243 (A) ORGANISM: primer C to Bovine Activin WC

244

245 (ix) FEATURE:

246 (A) NAME/KEY: misc_feature

247 (B) LOCATION: 1..9

248 (D) OTHER INFORMATION: /note= "Restriction site for XbaI"

249

250

251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

252

253 TAGTCTAGAT GCTCCGGCCA GTGCGAGTAC

254

255 (2) INFORMATION FOR SEQ ID NO:6:

256

257 (i) SEQUENCE CHARACTERISTICS:

258 (A) LENGTH: 30 base pairs